```
   1 CTGGCTCCAG GTCTGACTCA GTCCACTACA AGCTAGACGG TCTTCTTAAA
  51 GCACCAACAT TACTTGAGTC TTTGGATAAA ATTGAGAAAA GAGTCTACAA
 101 GTATTGTGGA CTCTACAGGA GGCAGGAGGC TGACAACTGG CAGTAAAGAC
 151 AAAGATGTCA GGCCTGCGGC CCGGCACTCA AGTGGACCCT GAGATTGAGC
 201 TTTTTGTAAA GGCTGGAAGT GATGGAGAGA GTATTGGAAA CTGTCCCTTT
 251 TGCCAACGCC TTTTCATGAT CCTCTGGCTT AAAGGAGTTA AATTTAATGT
 301 GACAACTGTT GACATGACCA GAAAGCCTGA AGAACTAAAG GACTTAGCCC
 351 CAGGTACCAA TCCTCCGTTC CTGGTGTATA ACAAGGAGTT GAAAACAGAC
 401 TTCATTAAAA TTGAGGAGTT TTTAGAACAA ACCCTGGCTC CTCCAAGGTA
 451 CCCTCACCTG AGTCCCAAGT ACAAGGAGTC TTTTGATGTG GGCTGTAACC
 501 TCTTTGCCAA GTTTTCTGCA TACATTAAGA ATACACAAAA GGAGGCAAAT
 551 AAGAATTTTG AAAAATCTCT GCTCAAAGAA TTCAAGCGTC TGGATGACTA
 601 CTTAAACACC CCACTTCTGG ATGAAATTGA TCCAGACAGT GCTGAGGAAC
 651 CCCCAGTTTC CAGAAGACTA TTCTTGGATG GGGACCAGCT AACACTGGCT
 701 GATTGTAGCT TGTTACCCAA GCTGAACATT ATTAAAGTTG CTGCCAAGAA
 751 ATATCGTGAC TTTGACATTC CAGCAGAATT CTCAGGAGTC TGGCGTTATC
 801 TCCACAATGC CTATGCCCGT GAAGAATTTA CCCACACGTG TCCTGAAGAC
 851 AAAGAAATTG AAAATACTTA CGCAAATGTG GCTAAACAGA AGAGTTAGGA
 901 GAGCTCTTAC AGGAGAAAAG GCTATATTTG TGATCAGATT TTACTTATTG
 951 ACATATTAGA AAGGTTTTTG CAAATAAGAA TATGAAAAAT ACTGTTTCTT
1001 CTATCCAACT CTCTTATGAA AAGGAACTCT GTATTTTCTA TTAGCCATAA
1051 ATAATCTGTC CACTGTATTT TACAGGTCTT CATACTTTTA CTTAATTTTC
1101 TTTATCTGTA TGGCAAACCA CTGCAATCCT GAATGACATG GAAAGCATCA
1151 CAATCTTTTG CCCTTTGCTT GAATTCCTGG AATGCATACA TATAAGCTAA
1201 ACAGATGTCT GCAGTTATAA ATGTCATAAG TAGAGGTACA ATCTCACCCT
1251 GCTCCTTAGA AACATTTCCA TATAAATCGC TAAAATAATT TCACATTTTT
1301 GTTAGTTTAA TATATACATG AGTTTATTTC TGATATAAAT AATAAATACA
1351 GAGAGTGAGC ATATCAGAGA GGCAAATTCT TAAAGAATGA TTTTTAAAAT
1401 CAGCTCTAGG AAGAGCTCAA GATCAATTGG TCATAGAACA GCATTTGACG
1451 CCTAGAACTA TGACCACCTC ATGGTCAGAG ATGAGAATGT AGCCTTTGTG
1501 ACCAGATTAT ATTATTTTTA AATGAAGAAG CACTCATTAA ATAAAACATA
1551 ATTTTAAAAA ACAATATAAG AAACAAAGTC AACTGAATCT TTTATTCATA
1601 GAAATGAAAA GGAAAATAAA AACTGTGGCT GACCAAAAGG TCTTCTTGTT
1651 GTCCATAAAA GGATAAGGTA AACAGTCCTT AGATAATTAC AAAACTTTCT
1701 ACAAAAGTTA AAATGTTACA TTACTATACG TATTCAGATT CACTTGTTAA
1751 AGTACTCTTA AATCATTCAA ATCTGGAAAC AAAAGCTGAA CTTAACTCTT
1801 GCTCCCTCAA AAGAGAAACA CAAGCATAAG TGCAGCTTCA AAAAAGGAAA
1851 ATATTTTAGG CTTTGGTGGA AGGGTGGAGT TTAGATAAAA TTTAAATGAA
1901 GTAGCGTTTT AATAGGTTCA AAGAAAAGTA AGGCAATGAG CAAACTCAAA
1951 GTACTGTCCT TGAAAACCAT AGAGTCAAGA TAAATGTATA GTGTATGGTT
2001 AGGTGGCAGA GAAATGCAAT CATGTTGATA ATCTTTGAGA TACATCCTGT
2051 CATCAGTATA TTTCAGAATA CATGCAATGC ACTAGCAAGT TACAATTGAT
2101 AGAATACATT TGAAATGTTA AATGAAATAA GCCAGGCACA GAAAGACAAA
2151 CACCACATGA TCTCACTCAT ATGTGGAATT TTAAAAAGTT GATCTCACTC
2201 ATATGTGGAA TTTTAAAAAG TTGATCTCAC ACAAGTAGAG GGTAGAATCG
2251 TGGTTACCAG GGGCTAGGGA GAGAAAGAAG GCAGAGGCAC TGAAAGATGT
2301 TGGTCAATGG GTATAAAGTT ACACCTAGGA AGAATAAATT TTGGTATTCA
2351 CCACAGTAGG GTGACTATAG CAAATAATAA TGTAGCATGT ATTTCAAGAT
2401 AGCTAGAAAA GCAGGTTTTT AAATGTCACC ACAAAGAAAT AACAAATGTT
2451 TATAGTGGTG GATATGGTAA TTACGCCTAT TTGATCATTA TACTGTGTGT
2501 ACATGCATTG AAACACCACA TTGTATCCCA TATATATGTA CAATTATGTG
2551 CCCATTATAC ATTTAAAAAA TAAATTTTAA AAACCTTCAA AAAAAAAAAA
2601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2651 AAAAAAAAAA AA  (SEQ ID NO:1)
```

FEATURES:

5'UTR:	1-154
Start Codon:	155
Stop Codon:	896
3'UTR:	899

FIGURE 1, page 1 of 2

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CRA|18000005108129 /altid=gi|4557020 /def=ref|NP_001280.1| chlo...	505	e-141
CRA|18000005108132 /altid=gi|3121853 /def=sp|O15247|CLI2_HUMAN ...	504	e-141
CRA|1000682328819 /altid=gi|7330335 /def=ref|NP_039234.1| chlor...	334	3e-90
CRA|18000005238101 /altid=gi|6685319 /def=sp|Q9Y696|CLI4_HUMAN ...	334	3e-90
CRA|103000001516844 /altid=gi|8393147 /def=ref|NP_058625.1| chl...	334	3e-90
CRA|1000685680369 /altid=gi|7304963 /def=ref|NP_038913.1| chlor...	333	4e-90
CRA|268676875 /altid=gi|7592636 /def=dbj|BAA94345.1| (AB035520)...	332	1e-89
CRA|18000005208220 /altid=gi|6685295 /def=sp|Q9Z0W7|CLI4_RAT CH...	330	7e-89
CRA|18000005222663 /altid=gi|4588524 /def=gb|AAD26136.1|AF10919...	328	2e-88
CRA|335001114793760 /altid=gi|12232044 /def=gb|AAG49367.1|AF323...	326	6e-88

BLAST dbEST hits:

	Score	E
gi|3597999 /dataset=dbest /taxon=9606 ...	1063	0.0
gi|10971515 /dataset=dbest /taxon=96...	827	0.0
gi|4630214 /dataset=dbest /taxon=9606 ...	823	0.0
gi|9867186 /dataset=dbest /taxon=960...	646	0.0
gi|1295759 /dataset=dbest /taxon=9606 ...	607	e-171
gi|1950308 /dataset=dbest /taxon=9606 ...	605	e-171
gi|3752728 /dataset=dbest /taxon=9606 ...	543	e-152

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|3597999 uterus
gi|10971515 lung
gi|4630214 germ cell
gi|9867186 liver
gi|1295759 parathyroid gland
gi|1950308 prostate
gi|3752728 placenta

From tissue screening panels:

Whole liver

FIGURE 1, page 2 of 2

```
   1 MSGLRPGTQV DPEIELFVKA GSDGESIGNC PFCQRLFMIL WLKGVKFNVT
  51 TVDMTRKPEE LKDLAPGTNP PFLVYNKELK TDFIKIEEFL EQTLAPPRYP
 101 HLSPKYKESF DVGCNLFAKF SAYIKNTQKE ANKNFEKSLL KEFKRLDDYL
 151 NTPLLDEIDP DSAEEPPVSR RLFLDGDQLT LADCSLLPKL NIIKVAAKKY
 201 RDFDIPAEFS GVWRYLHNAY AREEFTHTCP EDKEIENTYA NVAKQKS  (SEQ ID NO:2)
```

FEATURES:
Functional domains and key regions:

```
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

            48-51 NVTT

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 4
      1      55-57 TRK
      2    103-105 SPK
      3    127-129 TQK
      4    169-171 SRR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 7
      1       8-11 TQVD
      2      22-25 SDGE
      3      50-53 TTVD
      4    127-130 TQKE
      5    162-165 SAEE
      6    180-183 TLAD
      7    228-231 TCPE

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

           233-239 KEIENTY

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2
      1        3-8 GLRPGT
      2      44-49 GVKFNV
```

FIGURE 2, page 1 of 2

BLAST Alignment to Top Hit:

>CRA|18000005108129 /altid=gi|4557020 /def=ref|NP_001280.1| chloride intracellular channel 2 [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=243

Length = 243

Score = 505 bits (1286), Expect = e-141
Identities = 242/243 (99%), Positives = 242/243 (99%)
Frame = +2

```
Query: 155 MSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLFMILWLKGVKFNVTTVDMTRKPEE 334
           MSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLFMILWLKGVKFNVTTVDMTRKPEE
Sbjct: 1   MSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLFMILWLKGVKFNVTTVDMTRKPEE 60

Query: 335 LKDLAPGTNPPFLVYNKELKTDFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKF 514
           LKDLAPGTNPPFLVYNKELKTDFIKIEEFLEQTLAPPRYPHLSPKYKE FDVGCNLFAKF
Sbjct: 61  LKDLAPGTNPPFLVYNKELKTDFIKIEEFLEQTLAPPRYPHLSPKYKECFDVGCNLFAKF 120

Query: 515 SAYIKNTQKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVSRRLFLDGDQLT 694
           SAYIKNTQKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVSRRLFLDGDQLT
Sbjct: 121 SAYIKNTQKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVSRRLFLDGDQLT 180

Query: 695 LADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEDKEIENTYA 874
           LADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEDKEIENTYA
Sbjct: 181 LADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEDKEIENTYA 240

Query: 875 NVA 883
           NVA
Sbjct: 241 NVA 243  (SEQ ID NO:4)
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FIGURE 2, page 2 of 2

```
   1 AGAACTAATC ATGGTTCCTG ATACAGACGC CAAAACAAGG AAGTGATCTG
  51 TTCCAGTCCA AGCTTCCAAG AAATAAAGAA CTAGGTGGGG CACACTAAAC
 101 AAGCCCCCAG ACTCAACCAC CCCAGTGAAC ATTCCCTGGT TGTAGAGAGA
 151 AGTGAAATTT GCAACCCAGA ACAGAAATCT GGCTGTGTGA GCAGTAGGAT
 201 TGGGGGTGGA AACATTTAAT GAAGTACAAT TTTTTAACCC TCTTTTAGAC
 251 AGTATCACTG GATAAACATC CTTTTCAATA ATAAAAATCC AAGTCATTTC
 301 TGGCCCTTTT CCTGGAAGTG CTTTCAAGTT ACAGGAACAC CAATAAGAGG
 351 CCCTTTTCTG GGCATGGAGC CCAGGTCTCA AAGGGAGGCT CTAGAAAACA
 401 TCTGGTCTGC TTGATATATA GAAACTAGCA CTGCATGTGT GTGTTTCTGT
 451 GCATGTGTTT CTCCTGTGCT GACTCATGGC ATTGAAGCCT CTCTGGAAAC
 501 ACCCCCACCC TTCTAGCCAG GCAGTTTATA CACACCCCTT TGGCTCCTCC
 551 TTGATTTAAA TGTTAGATCA CGAGGAAGAA GGAAAACGAT TTCAAGAGCT
 601 GCACTTAAGC ATCTAGAATT TTCTGCGTCA CACCTCTTGA GAGAAGAGAC
 651 TGGCTCCAGG TCTGACTCAG TCCACTACAA GCTAGACGGT CTTCTTAAAG
 701 CACCAACATT ACTTGAGTCT TTGGATAAAA TTGAGAAAAG AGTCTACAAG
 751 TATTGTGGAC TCTACAGGAG GCAGGAGGCT GACAACTGGC AGTAAAGACA
 801 AAGATGTCAG GCCTGCGGCC CGGCACTCAA GTGGACCCTG AGATTGAGCT
 851 TTTTGTAAAG GTAAGTTTTC CAGTTATAAT AACTGCATGT AGAATATATT
 901 AGTTTTTGAC ACTGAAGTCC AATGTCTTTA AAAATTCTCC ACATTTGGGC
 951 TAGAGATAGG AAAGAATGTT GTGATTATTT TCCTACTCTG AGTTCTAGAA
1001 GAATGCCCGG GTGTGTGACT GTTCTTAGAT GACAACAGGA AAACAGATCT
1051 CTTCTGAAAA AGGCAAGGTG ATATGGTGGA AAAGCACTAG ACTGGTTTGT
1101 AGTGAGCGAC TAAATTATAT TCTTAATGGC TTCCTATATA ACCTTAGAAA
1151 AATCCCTCCT TCTCTCCAGA CTTTTTTTTC TCCATCTATA CAATGAAGGA
1201 GCATGACAAG ATGATCCTTA AGGGCTTTCC AAGTCTCAAA ATCTGTGTTT
1251 TATGAGATAG GTTTTGGAAG GCCTGACTGG GTGGAGGAGA GGGCCGAGAA
1301 TGACCTGAGA ACTCCATTCC CACACATAGC CTAGACAGAA CTTTCTAAAC
1351 TTCTACAATG GACAAACATC ACAGCAGGGT CACATGGACA CTGGGAGAAA
1401 AAAAACAGGA GTCTGTGTGC TTGTTATGTG AGGAGGGGGA CATTTTAGAA
1451 TGCTCTGCTT CTTCTTTTTG GTCTGCCATG GAGTTGTTTT TTTTTTTTTT
1501 TAACATGTCA ACTTTTCAGA AAAGCACTTT GGAAAACCCC TAAATCAAGA
1551 GAAAGGAACA TGTGTTTCCA AATTAGCTCA TCAAGAAAGA AAAATTTATA
1601 TGGGTTATTC CCAGTAGAAA TTAAACAGCT TACTAAATCC TCGCTTACAT
1651 TAACTGTGTA GCTTTTCCCT TTATTTTCAC TGACTATTGG ATAGTATTCA
1701 GGATAATAAG AACAATAACA AACTCATATT GTGCCTGGCT CTTTTCTAAA
1751 TACTTTACAT ATGTTACCTA ATTTAGTCCT AACAACTTAG GAGATAGGTT
1801 GTTATTAATG GTGCTTGTAT AGTACTAGCA TCATCAGTAG TAGTAGTGAT
1851 AGTAGTAGTT ATTACTACTT CATTACAACT TTTAGTTATT ACAATATTAT
1901 AATGTTGTTC TCATCATTTC TAGATAGGTA AACTAAGGCA TTAAAGTTTA
1951 AGTAACTTGC CTCTAAAACT ATACAGCTCC CTGATGGCTT ACAAAGACAT
2001 AAAATAAGAT ATACTTACCA AATGTTAAGT TAAATACCTA TTGGCAAAAG
2051 TAATGCTTTT ACAGCCAGTT AGATTATTTA ACAGCTTGTC ACATATATAC
2101 ACCAAGGACA TCATCAACCT GTCTTTTCAA AATTGTAAGA GAAAGACCCT
2151 TGAATTCCTG CAGTGCTAGG TAATGCAATT AAGTGTTTGC TAAACTATCG
2201 GGCATAAGAG CGACTTCTTC TATCTCTGGG TTGTAGCAAA ACATATAACT
2251 GCTCAGATAG GATATAAATG AGCTGTAATT TCCTAACTGG CTTTTTACAT
2301 TTACCAATTC CAAATCAGAA GTAATGTCTC TTCACTGGGT AACTAAAGTG
2351 TTCCCTTTGT CTGAACTGTT CATTCAACTC AATTAGACTC CTGAAATCAA
2401 TTGTTGGCTT TCACCTATGT GTTTATCTTC ATAGACTTTT CATATTTGGG
2451 TGGTAATCTG GACAGGAAAC TTTAGCAAGT CACACATGGA TGAGAAAATG
2501 TTGAATTAAA TAATAACTTT CAAAGGAACC AATAATTTAT TGAGTACTTA
2551 CTATATGGTA GGCACTGTGC TAAGTGGTTT ATTAACCCTC TTTTATGAAT
2601 ACAGAAATTA AAGCAAAGAG CAGCTAAGTA ACTTTGTCCA AGGTCACATA
2651 GCTAGTTAGT GGCAGAGTTA GAATTCTATT CCTTTAAAAT AGCTATGTCT
2701 AATATTATTC AATTGTTTTC AGTTGTGTGA ACTTTTTAGT AAACTAGTCC
2751 AGAATTTTAT CAGGTGGAGT GCTTTAGATG TAAGCTTATC TAATGACATT
2801 GATACAAATT ACAGATTTTC TGGAAGAACC TCAAATATCA TCTGGTCCAG
2851 GTTTTTGTTT TATTTTAAGC TGTGTTCCAC AGATCTCTAG AAGTTTCGTG
2901 GAAGATACTG GGAGGGGAAA TAGGGGTTGA GAAAGACTAA AAGTGCTAAT
2951 GAGTAATTTT TAAAAGGCAT TACTACAAGA GATTAAGCAT TCTCCTGTCA
3001 CAATTAAGAA TTTATACTAC GATATCTATG TGTTCTGTGT AGTCAATAAA
3051 AACATTGTCT TTTAGCTCTG AATGATTTGA GCAAGGTTTC TATCCAATAA
3101 CTAAGAACAA AGATTTCATA ACACACATTT TATTTTCTCT AAGTGTAGGG
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FIGURE 3, page 1 of 24

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3151 ATGAAATAAT CTTAATGATT TGTTGTTTGT TGTTAAATGG AATGTTTGCA
3201 TTCTGTACCA AAGACTCTAA AATTAAGTTT TAGTATATTT GTACATAAAA
3251 TTATGGAATT TAACATTTGG GCCAAAATTC TGAATGTAAT ACTTTTGTCA
3301 AAAACTTTTT TTAATGTGTG GGGGAAAGAA GGAAGAGATG ATACTCTACT
3351 CTGAGTGTTC AGACCATTTC AAAGTATCTT ATAGCTATTA TAAATACTTA
3401 TAAAGACTGA TTAATATAAA AATTCAACAA AACTATTAAA TGAGAGAAGG
3451 CAGTGTTTAA GAGTATGGTG TCTGGAGGAT ATAGTCCTGG TCCTGAATTT
3501 ACTGAGTGAG AAGAGGATGT ATGTCATCAA CTCTTGATTA GCCGACTGTA
3551 CTTGAGCAAG TCAGCCTCTC TGAGCCTCAG TTTCCTCACC TGTAAAACAA
3601 GTGTAATAAC AGAGCCTACC TCATAGCATC ATCCTATTTG TAAGGATTAA
3651 ATAAAACAAG TGTATAAAGC ACAGTAGTTG GCAATGTAGT AAACACTTTA
3701 TAAATGTTAA CTATTGTTGC CATTATTATT TTTCATGTTT AAAAACTTAG
3751 ATCACAAACA CAAAGAAAAA AATTGTTTTG GTGAATGGCT GCATCCTGTC
3801 TTTGCCAGCT GAAGATAATT AAGAGATCAG TAATTCATCA ATCAGGCTAG
3851 CGAATTTATA TCCTAAAATT GTATGTGATG GCACTTTAAA TCAGCATAAC
3901 ATAACAGAAA AAAAAACCCT TCAGTTTTCC TGTAAAACTT TACTGCATTT
3951 CCCCCACACC TCAGTGTTTT GATTTTCCTT TTGCCAAAGG CGATCCACCC
4001 TTCCTGCTGT ATCTATTATC AGACTCCATT CTTCTTCCTG CCTCCCACCC
4051 TTAATCATGT TTCCACTCAC TAAACCTAGT TTTGATTGGA TCCTTAGTCT
4101 GACTTCTATT ACAAAACAAA TGCAGCTGGT AAGGTTGGGT TGCCTCTTCC
4151 CCATTCCTCT TCACACCCTG CCATCATAAA GATCAACAAT ATCATTTTCT
4201 TTGTCACATC CACTATCAGG GAAAGAAAAT TTTGTCAAAA AATTGAAATT
4251 TTGTCCAGTG TTTCTGGACC TTAATAATTC TACGCATAAT AGATCAGAGC
4301 AGCCGTAAGA TGAAGTACCT TTTATTTCCT TCTATAGGCT ACTCTCTCTA
4351 GTCTTTCCTA TCATAATTCT TGGTGATTTT AATATCTACA CAGATGATTC
4401 TTCCAACACT CTAGCCCCTC AGATCCCTGA CTTTCCCTCC TCCAGGGATC
4451 TTAGTCCTCA TCATCTCTCA GGTGCTTCTT CCCATAGTCA TACGCTTACC
4501 TTTGTCATTG CAATGTCTGC AACCTCTGCA TAATATCATT TATTTGGGGG
4551 TGTTTTTTGT TCTTCTTTTT GAACTTCTCT ATTTTCATAG GTACATGTTT
4601 AACTTTGACA AAATACTTTA AAAAGCAGTT GTACCATTTT ACACTTCACT
4651 TCATTATGTG AGAGTTCCAC TTGCTCCACT TTCCTGTCAA CACTTGGTAT
4701 GGTCATTCTT TTTCATTTCA GTTATTCTAA TGTGTTTATC ATGGTATCTC
4751 ATTGTGGTTT TAATTTGCCT TTCCCACATG TCTAATGATA TTGGGCATCT
4801 TTTCATGTCC TTATTTATCA TCTGTATATC TTCCTTTGTA AAGTTTTCAA
4851 ATCTCTTCCC CATTTTAATT GTTCTTTAAC TTTAATTTTT AATTTTTGTG
4901 AGTACATAGT AGGTATATAT ATTTATGGGT TGCATGGAAT ATTTTGATAC
4951 AGGCATGCAA CATGTAATAA TCACATCAGG TAAATGGGAT ATTCATCCCC
5001 TCAAGCATTT ATCTTTTGGG TTACAAACAA TTCAATTATA CTGTTTTAGT
5051 TATTTTTAAA TGTACAATTA AATTATTTTT CACTGCAGTC ACCTTATTGT
5101 GCTAGCAAAT ACTAGGTGTT ATTCATCCTT CCTAGCTATT TTTTGTACCC
5151 ATTAACACTC TTCACCTCCC CACACACACA GACTCACTAC CCTTCCCAGC
5201 CTCTAGTAGC CATCCTTTAC TCTCTCTATG AGTTCAAATG TTTTTGTTCT
5251 TAGCTCTCAC AAATAAGTGA GAACACGTGA AGTTTGACTT CTGTGCCTGG
5301 CTTATTTTAT GTAATATATG ACGTCCAGTT CCATCCATGT TGTTGCAAAT
5351 GACTGAATCT CATTCTTTTT TATGGTTGAA TAGTACTCTG CTGTGTATAT
5401 GCCCACATTT TCTGTATCCA TTCATCTGTT GATGGGATAT TTAGGTTGCT
5451 TCCAAATCTT GGCTATTGTG AATAGTACTG CAATGAATGT GGGAGTGCNN
5501 NNNNNNNNNN NNNNNNNNNN NNNNNNNGCT GAGATGATAT CTCATTGTAG
5551 TTTTGATTTG AATTTCTCTG ATGATCAATG ACATTGAGCA CCTTTTCATA
5601 TGGCTCTTCA CCATTTGTAT ATCTTCTTTT GAGGAATGTC TATTCACATC
5651 TTTTGCCCAT TTGTCAAACA CAGTATTAGA TTTTTTCCTA TAGAGTTATT
5701 TGAGCTCCTT ATATATTCTG GTTATTAATC CCTTGTCAGA TAGGTGGTTT
5751 GCAAATACTT TCTCCCATTC TGTGGGTCGT CTTTGCACAT TGTTGATTCC
5801 TTTGCTGTGC AGAAGCTTGT TAACTTGATG TGATCCCATT CGTCCATTTT
5851 TGCTTTGCTT GCCTGTATTT ATGGCATATT ATTCAAGAAA TCTCTGCCCA
5901 CTCCAATGTC TTGGAGAGTT TCCCTAATGT TTTCTTTTAG TAGTTTCATA
5951 GTTTCAGGTC TTAGATTTAA GCCTTTAATC CATTTGTATT TGATTTTTTG
6001 TATATGGTGA GAGATAGGGG TCTAGTTTCA TTCTTTTGCA TATGGATATC
6051 CAGTTTTCCC AGCACCTTTC CCCAGTGTAT GATCTTGGCA CCTTTCCTGA
6101 AAATGAGTTC ATTGTAAATG TATAGACTTA TCTCCAGGTT CTCTATTCTT
6151 TTCCACTGAT CTATGTGTCT TTTTTTATGC CAGGACCATG CCATTTTGGT
6201 TACTATAGCT CTGTAGTATA ATTTGAAGTC AGGTATTGCT TAGGAGATAG
6251 CTTTGGCTAT TCTGGGTCTT TCCTGGTTCC ATATAAATAT TAGGATTTTT
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6301 AAAAATTTCT GTGAATATAT GTCTTTGTCA TTTTGATAGG GATTGCATTA
6351 AATCTATAGA TTGCTTTGGG TACTATGGAC ATTTTAACTA TATTTATTCT
6401 TCCAATTCAT AAATATAGAA TATCTTTCCA TTTTTGTATG TCTTTTTCAA
6451 TTTCTTGTAT CAATGTTTTA TAGTTTTCAG GTAGAAATCT TTTAGTATTT
6501 TTGTTAATTA CTATGTACTT TATTTCATTT GTAGCTATTG CAAATGGAAT
6551 TACTTTCTTG ATTTTTTTTC ACATTGTTCA CTGTTGGCAT ATAGAAATGT
6601 CACTGATTTT TGTACGTTGA TTTTGTAACC TGCAACTTTA CTGAATTTAT
6651 CAACTTTAAG AGTTTTCATT GGAGTGTTTA GGTTTTTCCA AATATAAGAT
6701 CATATCATCT GCAAACAAGG TAATTTGACT TCCTCCTTTC CAATTTGGAA
6751 GCCTTTTTAT TTCTTTATCT TGTCTGATTG CTCTGGCTAG GACTTCCAGT
6801 ACTATGTTGA ATAACTGTGG TGAAAGTGGG CATCCTTGTT ATGTTCCCAA
6851 TCTTAGAGGA CAGGATTTCA GTTTTTGTCC ATTCAGTATA ATACTAGCTA
6901 TGGGTTTGTC ATATATGGCT TTTATTCTGT TGAGGTATGT TCCCTCTATA
6951 CCCATGTTTT TGAGGGTTTT TTGTCATAAA GGGATGTTTA ATATTATCAA
7001 ATGCTTTTTC AGCAACAATT AAAATGATCA TGAGGTTTTT GTTCTTCATT
7051 CTGTTGATAT GATGTATCTC ATTAATTGAT GTGTGTATGT TGAATCATTC
7101 TTGCATCACT GGAATAAATT GCACTTGGTC ATGATAAATG ATCTTTTGTT
7151 TTGTTTTTGT TTTCACTTTT AAGTACAGGG GTACATGTGC AGATTTGTTA
7201 TATAGGTAAA CTTGTGTCAT GGGTGTTTGT TGTACAAATT ATTTCATCAC
7251 CCAGGTATTA AGCCTAGTAC CCATTAGCTA TTTTTTTTTC TGAGTCCATG
7301 TATTCTCATC TTTTAGCTGC CACTTGTAAG TGAGAATGTG TGGTATTTGG
7351 TTTTCTGTTG CTGCATTAAT TTGCTAGGGA TAATGGCTTC TAGCTCTGTT
7401 CATGTTCCTA TAAAGGACAT GATCTCATTC TTTTTTAAAA AAGTGACTTT
7451 ATTTTATTTT AGTTACATAA ATTACAAAAT ATCACTAAGT GAAAATAAAA
7501 TCAATAAAAA TCATCCATGA TACCACCCAC TTTAACATTT ATGTGTATAG
7551 CCTCTTATGC TTTATTTCCT CACATATATA GATAAATACA TTCATCAAAA
7601 AGAGGTTATT TCATATATTA AGTTGGTACA AAATTAATTG CGCTTTTTGC
7651 CATTACTTTT AATACATTGT TTTGCAAACT ATTTTTATTT CACAATATAT
7701 TATGAATTTA TTTCTATAAC ATTAAATATA TTATCTGTAT GTATGTGTGT
7751 CTTGGTTTCT TATGACTAAA ATTTTTTAAA ATTAAGGCGT TGTTATGTTG
7801 AGATAGTTGA AGATTCACAT GCAGTTTTAA GAAATAATAC AGAGAGATGC
7851 TGTGTGCCCT TTACCAAGTT TCCCTTAATG ATAACATCTT GTAAAACTAT
7901 AGTATGATAA GAAAACCAGG ACATTATTGA CATTGATGCA GTCAGATACA
7951 GAAGATTTTC ATCACTACAC AGATCCGTGT TGCCCTTTTA AAGCCACATC
8001 CACTTGTGTC TCATCCAGTC CCTCAACCAT TAATCTCTTT TCTGCTTTGA
8051 TAATTTTATC ATGTCAAGAA TGTTACGTAA ATGGAATAAA ACAGTATATC
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21601 AACTTTGACA GTAGTTTTGT TTTTTTTTTT TTTTTTTTGC CTTATTTATA
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21701 GCTCAAGTGA TCCATCCTCC CTCCGTGGCA TCCCAAAGTG CTAGGATTGC
21751 AGGCATGAGC CATGGTGCCC AGCCTATTTT TGACTTTTTA ATCATAGCCA
21801 TTCTGACTGC GTGAGATGGT GTCTCATTCT GGTTTTGATT TGAATTTCTC
21851 TAATTATCAG GGGTGTTGAA CTTTTTTTTC ATACGCTCAT TGGCCACATG
21901 CATGTCTTCT TTTGAAAAGT GTCTATTCAT GTTATTTGCC CACTTTTTCA
21951 TAGGCTTTTT CTTGTAAATT TGTTTAAGTT TCTTATAGAT GCTGGATATT
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22401 ATTGGGGAAA AGACTCCTTA TTCAATAAAT GGTGCTGGGA TAATTGGCTA
22451 GCCCTATGCA GGAGGTTTAA AATGGACCCC TTTCCTACAC CATATACAAA
22501 AATAAACTCA AGATGGGTGA AGTACTGAAA TGCAAAATGC AAAAGTGCAA
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FIGURE 3, page 11 of 24

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34751 NNNNNNNNNN NNNNNNNNNN TCTGGGGACT GTTGTGGGGT GGGGGGAGGG
34801 GGGAGGGATA ACATCAGGAG ATATACCTAA TGCTAGATGA CGAGTTAGTG
34851 GGTGCAGCGC ACCAGCATGG CACATGTATA CATATGTAAC TAACCTGCAC
34901 AATGTGCACA TGTACCCTAA AACTTAAAGT ATAATAATAA AAAAAAAAGA
34951 AAGGAAATTT GGTAAGATCT ATCAAAATGG GAAATGTGCA TACATTTTAC
35001 TGACCATTTT CATTTTAAAG ATTAACCTTA AAGATATAAT CTCAGAAGTG
35051 GAAGAAGCTA TATGCCCAGA AATGTTTGTT TCTGAAGTGC TTAGAGTAGT
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35151 TCTGATAATA TATAAAATTT ATTATTATTA TTATGTACCC ATCACAGTTG
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35251 AGATGATGGA GTACATGAGA TTAAGAATGT CCATGTTTGT CTCTAGCAAC
35301 TGGCTCATTT CCTATTAGGA ACTAAATACA TACTTATTGA ACAAACAAAT
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35701 AATTGAGGAG TTTTTAGAAC AAACCCTGGC TCCTCCAAGG TACAGCATTT
35751 ACAAGATACT ATTTTGCTGA AGATAATCTA TTTTACTGGC TTGTTTATTG
35801 CAGATTTAGT ATTCTTACCA ATTTAAGTAC TTTTGGATTT CTGGGCCTAC
35851 ATGTCAAATG ACACACATGC ATAAACATAC CCCTCCAACT TCAAATACAA
35901 AAAGATGATA TGTGTAATAT TTCAAATAAT TTTTAAAAGC TGCATAACAT
35951 ACATAACACA AGAAGGTAAG TTCTCTGTGC TCTAGAAATA GAGTAGGAAC
36001 ATATAGTGAG ATGGGAGTGA GGGAATGGGA TACTAACACT ATGTAATTCA
36051 TAAGGATTGG TCATGACTGG TCCTTAACAC CACTGACGAA ATGACAGAAC
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36151 AGAGGCCAGA ACTGTACTGC CACACTGAAT GACAACCGCA CATCTCTGTC
36201 TACCCAGGAT AGGTCTAGAA ACAAGAAGCA TGCTGTATTA ATTTTCTATT
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36301 ATTATCTCAC AGCTTCCATT GGTCAGTTGT CTGGGCATAG CCTGCTAAGG
36351 TCCTCTGCTG AGGGTATCAA AAAGTGGCAT TCAAGGTGTT GGTCGGGAAC
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36551 CTCTGTATAG GCATTTCGCA ACATGGCTGA TTGTTCTCTT CCTCTAAAAC
36601 CTGCAGGAGA ATGTCTCTCT GATGGTTCAC CTTCTTTTTT TTTTTTTTTT
36651 TTTTTTTTTT GAGACCGGAG TCTCGCTCTG TCCCCCAGGC TGGAGGGCAG
36701 TGGCACATGT TGGCTCACTG CAAGCTCCCC CTTTCGGGTC TCGGGTTCAC
36751 GCCATTCTCC TGCCTCAACC TCCCGAGTAG CTGGGACTAC AGATGCCCGC
36801 CACCACGCCC GGGTAATTTT TTTTTTTTTT TTTTGGAATT TTAATAAAAA
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36901 TCCACCCGCC TCGGCCTCCC AAAGGGCTGG GATTACAGGC GTGAGCCACT
36951 GCGCCCGGCC TGATGGGTCC CTTTCTTTTA AATTTTTTTA TCAGCACAAA
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37201 TCCCAATCAC CCTCCCCAGT CTCTGTTATC TCTCTTTCCA TTCTCTATCT
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37551 TTGGATAAAT GCCAATTAGT GAGATTTTTG GATCTTATGG TAGTGCTACT
37601 TTTGGTTTTT TCAGAAATTC TCCATGCGTT TTCCATAGTG GCTATATTTA
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37751 TTGTCTATTT TTGTTTCTAT TGCCTGTGCT TTTGACATCT CAATCATAAA
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38001 CCAATGTTCT TGTGAACTTT GTCAAAGATC AGCTGGCAGT AAATATGTGA
38051 ATTTATTTCT AGGTTCTCTA TTCTGACCAT TGCTCTGTGT GTCTATTTTT
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38151 GTCAGGTAAT GTGATGCCTC TAGCTTTGTT CTTTTTGCTC AGAATTGCTT
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38451 GATTAAAATT ATTCCTAGAT ATTTTAATTT TTAGCTATTG TAAATGGAAT
38501 TGCCATCTTC ATTTCTTTTG TGGGTAGATC ATTATTGGTG TATAGAAATG
38551 CTACATATTT TTTAGTGTTG ATGTTTTTAA CCTGGAACTT TACTGAATTT
38601 ACTTATCAAA TCTAAGAATT TTTTGGTGGA GTTTTTAGGT TTTACTAGAT
38651 ACAAGATCAT GGCACCAGTA AAAAGGGACA ATTTTACTTC CTTTTTCCCA
38701 ATTTGGATGC CTTTTATTTC TTTCTCTTGC CTGATTGCCA TACCTAGGAC
38751 TTCCAATACT ATGTTGAATA GGAGTGGTGA AAGTGGGCAT TCTTGTTTTT
38801 TTCCATTTCT TGGAGGAAAG GCTTTCAATT TTTCCCTATT CAGCATGATA
38851 TCAGCTGTGG GTTTGTCATA TATAGCCTTT ATTATTTTGA CATATTTTCC
38901 TTCTATGCCC CATTTGTTGA GAGGTTTTAT CATGAAGGGG TGTTGAATTT
38951 TATCAAATGC TTTTTCTGTA TCTATTGAGA TGATGATATG TTTTTTGTCC
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39251 TAAGGAGAGT TCTCTCCTCT TCCATTTTTT AGAATAGTTT CAGGAGAAAT
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39401 ATTATTGGTC TGTTCATGTT TTCTATTTCT TCCCAATTCA GTCTCAGCAC
39451 ATTGTATGTT TCCTGGAACT TATCCATTTC CTCTAGGTTT ATCAGTTTGT
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39551 ATATATGACT TAATGTGTCC TTTTTCATTT CTAATTTGTT TGTTTGGGTC
39601 TTCTACTTTT TTGGTTAGTC TAGCTGGCAG TTTATCAATT TAACAAAAAC
39651 CAACTTTTTC AATCATGATG CTTTGTATTT TTTAGTCTGT ATTTCATTTA
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40001 AGTTCCTCTT GGTGTTTATT TATAGTTGAT TTGATTTCAT TGTGGCCTGA
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40101 TGGCCTGACA TATGGTCCAT CCTGGAGAAT ATTCCATGTG CTGATGAATG
40151 TATATTCTGT AGTTGTTGGA TAGAATGTTC TGTAAATGTC TGTTTGGTTC
40201 ATTTGGTCTA AAGTCCAGTT TAAGTCTAAT GTTTATTTGT TGATTTTCTG
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40401 ATCTTTTTTG CTGGGTTGAT CTGTCATTAT ATAATGATAG TTTTAGTCCT
40451 TTTTTCACTT TTTTTGATTT AATGTCTGTT TTGTCTTATA TGATTATAGC
40501 TAATCCTGCT CACTTTTGGT TTCCGTTTGT GTGAAATATC TTTATCAACC
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40601 CTATGTAGTT GGATTATGTT TTTTAAGTCT ATTCATCCAG TGTATGTCTT
40651 TTAAGTGGAA TATTTAATCT GTTTATGTTT ACATGTGAAG ACTTATTTCT
40701 GTCATTTTGT TATTTTTTTC TGGTTGTTTT GTATATTCTT TGTTTTTTTT
40751 CTCTCTCTCT TGTCATTTAT CATTACAGTT TGGTGGTTTT GTGTAGTGGT
40801 AATATTTGAG TCCTTTATTT TCTTTATATC CAGGCAAGAA GGATGGCCAC
40851 TATTCTCACA CTGGGAGCAG TGTATAAGTG ATTCAGCCTT TCCTTTCTTG
40901 TTGGACTCCT TACCCTTCAG ACAAATTCCA CATATAGCAT TTGGAATGAC

FIGURE 3, page 13 of 24

40951 TTTGGGCTTG TACCCAGGAA CTGAGTTGGA CAGTACAGAA CGTTTGGGAG
41001 CATCTTTTCT TGGAGTGGCA GCTTTGTCTT TTGATTTCTG TCTTCCCTGG
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42551 CTTTACCTAT GTTGTTTGAT CATTTGGTTT TGTTCTCCTG TGAATCATAC
42601 TTGTCAAATA CCGTCTGATT TTCTATTAGC TTCATACTGA ATAGGNNNNN
42651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNTTTTC
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42751 GAGGCACAGG ACAAGGATGC CCTTCTTACC ACTCTTATTT AAAATAGTAT
42801 TGGAAGTTCT AGCCAGAGCA GTGAGGCAAG AGAAAGAAAT AATAGGGCAT
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42901 TTCCATATCT AGAAAACCCC ATACTCGGCT GCACTCAGCA TCGGAGCCAG
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43001 AGATGTTAAA GAGATCTTGC CAGAGCCAGA AATGGAAAGT ACAGACCTCT
43051 GAAAATATCT ATTGAAAATG GGCAACTTAT GATTGGATCA TATATAGTCA
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43201 GCCCAGGGAT ATGAATGGAT ATTCATTGCA TGGTTTCCAG ATCATTCTCA
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43401 TGCCCCACTG ACTGCAGCTG AGGAAGAATT ATGACATTAA ATCAANTGAG
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43951 AATTAGGGGC CCAGCGGAAA ATGAAGCTAC TACTGATTCA AGTCATCACA
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44051 AACTGAAATC ATTCCATGTT GATATAAAGT AGGGAAAAAA TTGTACTTTT

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44651 CCTTAGTAAA TTATCTAAGG CTCTGTGAAG CCAAACATTT ATGTTCAGAT
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47801 TCAAAGAGCT AACAGCAGAA CTACCATTTG ACCCAGCAAT CCCATTACTG
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48201 GAGGGTGGAG GGTTGGAGGA GGGAAAGGAG CAGAAAAGAT AACAACTGGG
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48301 TGACATGAGT TCACCTATGT AACAAACCTT CACATGTATC CGAAACTAAA
48351 ATAAATTTTT TTAATGAAAT AAATATGGTT TTTGGGGGGC CTCCTCTTTC
48401 GGCTTTGGAG CCCCCCTCCC TCTGTCTCGG TATGGGGGAG TTTCTTCCTT
48451 CTGTCTTCTC CCTTCCTTCT TGCCTATTAA ACTCTCCGCT CCTTAAAACC
48501 AAAATAAAAA AAAAAGAAAG AAAGAAATAT GGTTTTTATT TTTCTCACAT
48551 AAGAAACTCA GAATGAACCT AGGATGATAG CTCCGTAATT TCATTAGGGA
48601 TTTCAACTCC TAATCTTTCT TCTCTGCCAT CCTTCAAGTG AGGCTTCCAG
48651 TCTCAAAGTT AACTCATGGT GACAATATGT CTGCTGGAAC TCCAGGCAAC
48701 AGATCTAATA TACAAGCCAG CTCTAAGGAG TTTTCACAGA AGCCACACCC
48751 AAAAATTTCC ATTTACAGCT CATTGTCCAG AGGTAATTCA TGTGGTTAGA
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48851 CCACCCAAAT AAATGTATGT ATCCCTCTTC TCACATATGG AACACACAGT
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59401 GCACACCCAA TGCTAAGACC TTGGATTCTA ATATCATTCT CCAATA (SEQ ID NO:3)

FEATURES:

Start: 804
Exon: 804-860
Intron: 861-35378
Exon: 35379-35488
Intron: 35489-35613
Exon: 35614-35739

Intron: 35740-54281
Exon: 54282-54388
Intron: 54389-55020
Exon: 55021-55202
Intron: 55203-56286
Exon: 56287-56445
Stop: 56446

CHROMOSOME MAP POSITION:
Chromosome X

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain
7107	T	C	Intron
7202	A	T	Intron
8661	C	A	Intron
21620	T	-	Intron
27314	G	A	Intron
44327	T	A	Intron
44460	T	G	Intron
44877	A	G	Intron
46148	G	A	Intron
48158	C	T	Intron
48717	C	T	Intron
48970	A	G	Intron
49592	T	C	Intron
49826	G	C	Intron
52861	T	G	Intron
54703	T	C A	Intron
55624	G	C	Intron
56467	C	A	Beyond ORF(3')
57895	C	T	Beyond ORF(3')

Context:

DNA Position

7107
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[T,C]
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7202
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[T,C,A]
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